RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/567,074_

Source: _IFWP_

Date Processed by STIC: _02/21/2006_

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: _10/567,074_   CRF Edit Date: _02/21/2006_
                                     Edited by: _DA_

____ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

____ Corrected the SEQ ID NO. Sequence numbers edited were:

_____

____ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

_✓_ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

____ Inserted mandatory headings/numeric identifiers, specifically:

_____

____ Moved responses to same line as heading/numeric identifier, specifically:

_____

____ Other:

_____
_____
_____

Revised 09/09/2003

IFWP

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       5 <110> APPLICANT: Scherer, Stephen W.
       7        Minassian, Berge A.
      11 <120> TITLE OF INVENTION: Lafora's Disease Gene
      15 <130> FILE REFERENCE: 4012.1000-003
C-->  19 <140> CURRENT APPLICATION NUMBER: US/10/567,074
C-->  19 <141> CURRENT FILING DATE: 2006-02-03
      19 <150> PRIOR APPLICATION NUMBER: PCT/CA2004/001449
      21 <151> PRIOR FILING DATE: 2004-07-30
      25 <150> PRIOR APPLICATION NUMBER: US 60/491,968
      27 <151> PRIOR FILING DATE: 2003-08-04
      31 <160> NUMBER OF SEQ ID NOS: 5
      35 <170> SOFTWARE: PatentIn version 3.1
      39 <210> SEQ ID NO: 1
      41 <211> LENGTH: 2120
      43 <212> TYPE: DNA
      45 <213> ORGANISM: Homo sapiens
      49 <400> SEQUENCE: 1
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      52 atcagcctgc tcgagtgcaa ggtgtgcttt gagaagtttg gccaccggca gcagcggcgc     120
      54 ccgcgcaacc tgtcctgcgg ccacgtggtc tgcctggcct gcgtggccgc cctggcgcac     180
      56 ccgcgcactc tggccctcga gtgcccattc tgcaggcgag cttgccgggg ctgcgacacc     240
      58 agcgactgcc tgccggtgct gcacctcata gagctcctgg gctcagcgct tcgccagtcc     300
      60 ccggccgccc atcgcgccgc ccccagcgcc cccggagccc tcacctgcca ccacaccttc     360
      62 ggcggctggg ggaccctggt caaccccacc ggactggcgc tttgtcccaa gacggggcgt     420
      64 gtcgtggtgg tgcacgacgg caggaggcgt gtcaagattt ttgactcagg gggaggatgc     480
      66 gcgcatcagt ttggagagaa gggggacgct gcccaagaca ttaggtaccc tgtggatgtc     540
      68 accatcacca acgactgcca tgtggttgtc actacgccg gcgatcgctc catcaaagtg     600
      70 tttgattttt ttggccagat caagcttgtc attggaggcc aattctcctt accttggggt     660
      72 gtggagacca cccctcagaa tgggattgtg gtaactgatg cggaggcagg gtccctgcac     720
      74 ctcctggacg tcgacttcgc ggaaggggtc cttcggagaa ctgaaaggtt gcaagctcat     780
      76 ctgtgcaatc cccgaggggt ggcagtgtct ggctcaccg gggccattgc ggtcctggag     840
      78 cacccctgg ccctggggac tggggtttgc agcaccaggg tgaaagtgtt tagctcaagt     900
      80 atgcagcttg tcggccaagt ggatacctt gggctgagcc tctactttcc ctccaaaata     960
      82 actgcctccg ctgtgacctt tgatcaccag ggaaatgtga ttgttgcaga tacatctggt    1020
      84 ccagctatcc tttgcttagg aaaacctgag gagtttccag taccgaagcc catggtcact    1080
      86 catggtcttt cgcatcctgt ggctcttacc ttcaccaagg agaattctct tcttgtgctg    1140
      88 gacacagcat ctcattctat aaaagtctat aaagttgact gggggtgatg ggctggggtg    1200
      90 ggtccctgga atcagaagca ctagtgctgc cattaatgaa ttgtttaacc ctggataagt    1260
      92 cacttaaact catctatcca ggcagggata attaaaacca tctggcagac ttacaaagct    1320
      94 tgggacagtt attggagatt aatctaccat ttattgaatg catactctgt gcaaggaaat    1380
      96 ttgcaaatat tagcttattt aatctgtact atccagtgag gtaatttctt ccccccccag    1440
      98 atagagtcaa gctctgtcac ccaggctgga gtgcagaagc atgatcacag ctcactacag    1500
     100 tttcaacgtc ccccgctcag gtggtccttc cacctcagcc tcccaagtag ctgggaccac    1560
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RAW SEQUENCE LISTING   DATE: 02/21/2006
PATENT APPLICATION: US/10/567,074   TIME: 15:23:49

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\02212006\J567074.raw

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102 aagtgtgcat taccacactc agctaatttt tgtattttgg cagagatggg gtttcaccat  1620
104 gttgcccagg ctggtctcaa actcctgagt tcaagcaatc caccttcctc ggcctcccaa  1680
106 agtactagga gtacaggcat agccacttgc tcagccataa tttttattat taatctcatt  1740
108 gtacaagtga gaaaactgag acccagagag cttaagtgac ttcctcgagg tcatagttac  1800
110 ttactgcctt agtcccaatt tgaattcaat tctgattcca aataagttgc gcttaaataa  1860
112 gacaacagat gtgggaaaaa tatgtgaatg tgtagtgttg ctatgtgtac tgtctttaca  1920
114 agtagctaat tattttagca caaagatgtg caaagaaagg agactttatg gagagttcag  1980
116 gagaaaaagg attttgtggt ggccatcact ttcattcaat ttgcgactgc tctgatggca  2040
118 cattagatga agttactgtt gatcctgagt tacgtgaata agaaaaacaa ttgaactgct  2100
120 tattaaaaaa gtaaacatgt                                               2120
123 <210> SEQ ID NO: 2
125 <211> LENGTH: 395
127 <212> TYPE: PRT
129 <213> ORGANISM: Homo sapiens
133 <400> SEQUENCE: 2
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136 1               5                   10                  15
139 Arg Glu Ala Glu Ile Ser Leu Leu Glu Cys Lys Val Cys Phe Glu Lys
140             20                  25                  30
143 Phe Gly His Arg Gln Gln Arg Arg Pro Arg Asn Leu Ser Cys Gly His
144         35                  40                  45
147 Val Val Cys Leu Ala Cys Val Ala Ala Leu Ala His Pro Arg Thr Leu
148     50                  55                  60
151 Ala Leu Glu Cys Pro Phe Cys Arg Arg Ala Cys Arg Gly Cys Asp Thr
152 65                  70                  75                  80
155 Ser Asp Cys Leu Pro Val Leu His Leu Ile Glu Leu Leu Gly Ser Ala
156             85                  90                  95
159 Leu Arg Gln Ser Pro Ala Ala His Arg Ala Ala Pro Ser Ala Pro Gly
160             100                 105                 110
163 Ala Leu Thr Cys His His Thr Phe Gly Gly Trp Gly Thr Leu Val Asn
164         115                 120                 125
167 Pro Thr Gly Leu Ala Leu Cys Pro Lys Thr Gly Arg Val Val Val Val
168     130                 135                 140
171 His Asp Gly Arg Arg Arg Val Lys Ile Phe Asp Ser Gly Gly Gly Cys
172 145                 150                 155                 160
175 Ala His Gln Phe Gly Glu Lys Gly Asp Ala Ala Gln Asp Ile Arg Tyr
176             165                 170                 175
179 Pro Val Asp Val Thr Ile Thr Asn Asp Cys His Val Val Val Thr Asp
180             180                 185                 190
183 Ala Gly Asp Arg Ser Ile Lys Val Phe Asp Phe Phe Gly Gln Ile Lys
184         195                 200                 205
187 Leu Val Ile Gly Gly Gln Phe Ser Leu Pro Trp Gly Val Glu Thr Thr
188     210                 215                 220
191 Pro Gln Asn Gly Ile Val Val Thr Asp Ala Glu Ala Gly Ser Leu His
192 225                 230                 235                 240
195 Leu Leu Asp Val Asp Phe Ala Glu Gly Val Leu Arg Arg Thr Glu Arg
196             245                 250                 255
199 Leu Gln Ala His Leu Cys Asn Pro Arg Gly Val Ala Val Ser Trp Leu
200             260                 265                 270
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203 Thr Gly Ala Ile Ala Val Leu Glu His Pro Leu Ala Leu Gly Thr Gly
204         275             280             285
207 Val Cys Ser Thr Arg Val Lys Val Phe Ser Ser Ser Met Gln Leu Val
208     290             295             300
211 Gly Gln Val Asp Thr Phe Gly Leu Ser Leu Tyr Phe Pro Ser Lys Ile
212 305             310             315             320
215 Thr Ala Ser Ala Val Thr Phe Asp His Gln Gly Asn Val Ile Val Ala
216         325             330             335
219 Asp Thr Ser Gly Pro Ala Ile Leu Cys Leu Gly Lys Pro Glu Glu Phe
220         340             345             350
223 Pro Val Pro Lys Pro Met Val Thr His Gly Leu Ser His Pro Val Ala
224     355             360             365
227 Leu Thr Phe Thr Lys Glu Asn Ser Leu Leu Val Leu Asp Thr Ala Ser
228     370             375             380
231 His Ser Ile Lys Val Tyr Lys Val Asp Trp Gly
232 385             390             395
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237 <211> LENGTH: 3008
239 <212> TYPE DNA
241 <213> ORGANISM: Canis sp.
245 <220> FEATURE:
247 <221> NAME/KEY: CDS
249 <222> LOCATION: (698)..(1897)
251 <223> OTHER INFORMATION:
255 <220> FEATURE:
257 <221> NAME/KEY: misc_feature
259 <222> LOCATION: (2692)..(2692)
261 <223> OTHER INFORMATION: N=any nucleic acid
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277 <221> NAME/KEY: misc_feature
279 <222> LOCATION: (2750)..(2750)
281 <223> OTHER INFORMATION: N=any nucleic acid
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291 <223> OTHER INFORMATION: N=any nucleic acid
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301 <223> OTHER INFORMATION: N=any nucleic acid
305 <220> FEATURE:
307 <221> NAME/KEY: misc_feature
309 <222> LOCATION: (2916)..(2916)
311 <223> OTHER INFORMATION: N=any nucleic acid
315 <220> FEATURE:
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321 <223> OTHER INFORMATION: N=any nucleic acid
325 <220> FEATURE:
327 <221> NAME/KEY: misc_feature
329 <222> LOCATION: (2931)..(2931)
331 <223> OTHER INFORMATION: N=any nucleic acid
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337 <221> NAME/KEY: misc_feature
339 <222> LOCATION: (2941)..(2941)
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347 <221> NAME/KEY: misc_feature
349 <222> LOCATION: (2990)..(2990)
351 <223> OTHER INFORMATION: N=any nucleic acid
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356 ccccaaggcc cccccggccc ccaggcaacc ccaggcccc aggcaaccca aggcccccg     60
358 gccccaagcc ccccaggttc ccggccccaa gaaccaagcc ccccggcccc ccgcccccag    120
360 cacccagcac caagcccccg ccccccgccc caagcaccca gccccagcac ccagcccccg    180
362 ccccagcccc agccccagca cccagccccc gccccagcac ccagccccag cacccagccc    240
364 ccgccccagc cccagccccc gtccccccc ccagcaccca gccccagccc cagcagcagc    300
366 acccagcagg ggactgcaaa gcgtaggcta ccccaggtgg aacaccgtgt tctagttttg    360
368 ctttgccgtt tgcagcctgg gcgatcgggg gccaccgctc gagcctgttt cccgtcgcgg    420
370 aaagcggagc cgccccgccc cgcccccgc ctgcctgaag gtcacgggcc tgggcctgcg    480
372 gcgcgcggtg cggcccgcga gcgtccgctc ccgcgccctc cgcagtcagc gcccgcccgc    540
374 ccgccggggg accgcaggcc gcggccgaga ggctgcgcgc tgcgcccgcg acgtcaggcc    600
376 ccgccccgcc ccgccccgcc ccgtgaccgg ccccggcccc ggccccggcc ccggcccccgg    660
378 accgagcggc gcccgcggga gcggcggcgg ccgcgcg atg ggg gcc gaa gcg gcg    715
379                                             Met Gly Ala Glu Ala Ala
380                                              1                5
382 ggg agc ggg cgg gcg ctg cgg gag ctg gtg cgc gag gcc gag gtc agc    763
383 Gly Ser Gly Arg Ala Leu Arg Glu Leu Val Arg Glu Ala Glu Val Ser
384             10                  15                  20
386 ttg ctc gag tgc aag gtg tgc ttc gag agg ttc ggc cac cgc cag cag    811
387 Leu Leu Glu Cys Lys Val Cys Phe Glu Arg Phe Gly His Arg Gln Gln
388         25                  30                  35
390 cgg cgc ccg cgc aac ctg ccc tgc ggc cac gtg gtg tgc ctg gcc tgc    859
391 Arg Arg Pro Arg Asn Leu Pro Cys Gly His Val Val Cys Leu Ala Cys
392     40                  45                  50
394 gtg gcg gcc ctg gcg cac ccg cgg acg ctg gcc ctg gag tgc ccc ttc    907
395 Val Ala Ala Leu Ala His Pro Arg Thr Leu Ala Leu Glu Cys Pro Phe
396 55                  60                  65                  70
398 tgc cgc cgg gcc tgc cgc ggc tgc gac acc agc gac tgc ctg ccg gtg    955
399 Cys Arg Arg Ala Cys Arg Gly Cys Asp Thr Ser Asp Cys Leu Pro Val
400             75                  80                  85
402 ctt cac ctc ctg gag ctc ctg ggc tcg gcg ctg cgc cca gcc ccc gcc   1003
403 Leu His Leu Leu Glu Leu Leu Gly Ser Ala Leu Arg Pro Ala Pro Ala
404         90                  95                  100
406 gcc ccc cgc gcc gcc ccc cgc gcc gcc ccc tgc gcc ccg ggc gcc ctc   1051
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RAW SEQUENCE LISTING   DATE: 02/21/2006
PATENT APPLICATION: US/10/567,074   TIME: 15:23:49

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\02212006\J567074.raw

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407 Ala Pro Arg Ala Ala Pro Arg Ala Ala Pro Cys Ala Pro Gly Ala Leu
408         105                 110                 115
410 gcc tgc cat cac gcg ttc gga ggc tgg ggg acc ctg gtc aac ccc acg   1099
411 Ala Cys His His Ala Phe Gly Gly Trp Gly Thr Leu Val Asn Pro Thr
412     120                 125                 130
414 ggg ctg gcg ctg tgc ccc aag acc ggg cgg gtc gtg gtg gtg cac gac   1147
415 Gly Leu Ala Leu Cys Pro Lys Thr Gly Arg Val Val Val Val His Asp
416 135                 140                 145                 150
418 ggc agg agg cgg gtc aag atc ttt gac tcc ggg gga gga tgc gcc cat   1195
419 Gly Arg Arg Arg Val Lys Ile Phe Asp Ser Gly Gly Gly Cys Ala His
420             155                 160                 165
422 cag ttt gga gag aag ggg gag gct gcc cag gac att agg tac ccc ctg   1243
423 Gln Phe Gly Glu Lys Gly Glu Ala Ala Gln Asp Ile Arg Tyr Pro Leu
424             170                 175                 180
426 gac gtc gcc gtc acc aac gac tgc cac gtg gtt gtc acc gac gcc ggc   1291
427 Asp Val Ala Val Thr Asn Asp Cys His Val Val Val Thr Asp Ala Gly
428         185                 190                 195
430 gac cgc tcc atc aaa gtg ttt gat ttc ttt ggc cag atc aag ctc gtc   1339
431 Asp Arg Ser Ile Lys Val Phe Asp Phe Phe Gly Gln Ile Lys Leu Val
432     200                 205                 210
434 att gga gac cag ttt tcc tta cct tgg ggc gtg gag acc acc cct cag   1387
435 Ile Gly Asp Gln Phe Ser Leu Pro Trp Gly Val Glu Thr Thr Pro Gln
436 215                 220                 225                 230
438 aat ggg gtc gtg gta act gac gcc gag gca ggg tcg ctg cac ctg ctg   1435
439 Asn Gly Val Val Val Thr Asp Ala Glu Ala Gly Ser Leu His Leu Leu
440             235                 240                 245
442 gaa gtc gac ttt gca gaa gga gcc ctc cag agg act gaa aag ctg caa   1483
443 Glu Val Asp Phe Ala Glu Gly Ala Leu Gln Arg Thr Glu Lys Leu Gln
444             250                 255                 260
446 ggt cat ctg tgc aac ccg cga ggg gtg gcc gtg tcc tgg ctc act ggg   1531
447 Gly His Leu Cys Asn Pro Arg Gly Val Ala Val Ser Trp Leu Thr Gly
448             265                 270                 275
450 gcc att gcg gtc ctg gag cac cct ccg ggg ctg ggg gct ggg gcg ggc   1579
451 Ala Ile Ala Val Leu Glu His Pro Pro Gly Leu Gly Ala Gly Ala Gly
452     280                 285                 290
454 agc acc gcc gtg aag gtg ttc agc cca act atg cag ctg atc ggc cag   1627
455 Ser Thr Ala Val Lys Val Phe Ser Pro Thr Met Gln Leu Ile Gly Gln
456 295                 300                 305                 310
458 gtg gat acc ttt ggg ctc agc ctc ttt ttc ccc tct aga ata acc gcc   1675
459 Val Asp Thr Phe Gly Leu Ser Leu Phe Phe Pro Ser Arg Ile Thr Ala
460             315                 320                 325
462 tcc gcc gtg acc ttt gat cac cag ggg aat gtg att gtt gca gat act   1723
463 Ser Ala Val Thr Phe Asp His Gln Gly Asn Val Ile Val Ala Asp Thr
464             330                 335                 340
466 tct agt cag gcc gtc cta tgc ttg gga cag cct gag gaa ttt cca gtc   1771
467 Ser Ser Gln Ala Val Leu Cys Leu Gly Gln Pro Glu Glu Phe Pro Val
468         345                 350                 355
470 ctg aag ccc atc atc acc cat ggt ctt tcc cat cct gtg gca ctg acc   1819
471 Leu Lys Pro Ile Ile Thr His Gly Leu Ser His Pro Val Ala Leu Thr
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 02/21/2006
PATENT APPLICATION: US/10/567,074   TIME: 15:23:50

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\02212006\J567074.raw**

Please Note:
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.**

Seq#:3; N Pos. 2692,2748,2750,2793,2845,2916,2918,2931,2941,2990

VERIFICATION SUMMARY   DATE: 02/21/2006
PATENT APPLICATION: **US/10/567,074**   TIME: 15:23:50

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\02212006\J567074.raw**

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L:19 M:270 C: Current Application Number differs, Replaced Current Application No
L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:265 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:251
L:506 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2637
L:508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2697
L:510 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2757
L:512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2817
L:514 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2877
L:516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2937
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**Raw Sequence Listing before editing,
for reference only**

IFWP

RAW SEQUENCE LISTING   DATE: 02/10/2006
PATENT APPLICATION: **US/10/567,074**   TIME: 08:37:03

Input Set : **A:\40121000003.txt**
Output Set: **N:\CRF4\02102006\J567074.raw**

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   5 <110> APPLICANT: Scherer, Stephen W.
   7        Minassian, Berge A.
  11 <120> TITLE OF INVENTION: Lafora's Disease Gene
  15 <130> FILE REFERENCE: 4012.1000-003
C-->  19 <140> CURRENT APPLICATION NUMBER: US/10/567,074
C-->  19 <141> CURRENT FILING DATE: 2006-02-03
  19 <150> PRIOR APPLICATION NUMBER: PCT/CA2004/001449
  21 <151> PRIOR FILING DATE: 2004-07-30
  25 <150> PRIOR APPLICATION NUMBER: US 60/491,968
  27 <151> PRIOR FILING DATE: 2003-08-04
  31 <160> NUMBER OF SEQ ID NOS: 5
  35 <170> SOFTWARE: PatentIn version 3.1
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Does Not Comply
Corrected Diskette Needed
(p9-1)

ERRORED SEQUENCES

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 714 <210> SEQ ID NO: 5
 716 <211> LENGTH: 12
 718 <212> TYPE: DNA
 720 <213> ORGANISM: Canis sp.
 724 <400> SEQUENCE: 5
 725 gccgccccc gc
E-->  729 4012.1000-003
E-->  730 1/13
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→ deleted

12

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/567,074**

DATE: 02/10/2006
TIME: 08:37:04

Input Set : **A:\40121000003.txt**
Output Set: **N:\CRF4\02102006\J567074.raw**

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L:19 M:270 C: Current Application Number differs, Replaced Current Application No
L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:265 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:251
L:506 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2637
L:508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2697
L:510 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2757
L:512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2817
L:514 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2877
L:516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2937
L:729 M:254 E: No. of Bases conflict, LENGTH:Input:-3 Counted:14 SEQ:5
L:729 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
L:730 M:254 E: No. of Bases conflict, LENGTH:Input:13 Counted:15 SEQ:5
L:730 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:730 M:252 E: No. of Seq. differs, <211> LENGTH:Input:12 Found:15 SEQ:5
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